AMENDMENTS TO THE SPECIFICATION

Please insert the following new paragraph at page 1, line 25 in a separate paragraph before the section entitled "Background of Invention":

COMPUTER PROGRAM LISTING APPENDIX

Two copies of a CD ("Copy 1" and "Copy 2") containing the computer program listings of Appendix A and B are incorporated herein by reference. Each copy of the CD was created on March 19, 2004 and contains a file named APPAandB.txt (347 KB) and APPAandB.tif (5,150 KB).

Please replace the paragraph beginning on page 5, line 11 with the following amended paragraph:

Fig. 5[a]A and 5[b]B illustrate operation of a program for polymer synthesis;

Please replace the paragraph beginning on page 5, line 19 with the following amended paragraph:

Fig. 9[a]A schematically illustrates a masking scheme for a four step synthesis;

Please replace the paragraph beginning on page 5, line 21 with the following amended paragraph:

Fig. 9[b]B schematically illustrates a masking scheme for a four step synthesis;

Please replace the paragraph beginning on page 20, line 1 with the following amended paragraph:

Figs. 5[a]A and 5[b]B are flow charts of the software used in operation of the reactor system. At step 502 the peptide synthesis software is initialized. At step 504 the system calibrates positioners on the x-y translation stage and begins a main loop. At step 506 the system determines which, if any, of the function keys on the computer have been pressed. If F1 has been pressed, the system prompts the user for input of a desired synthesis process. If the user enters F2, the system allows a user to edit a file for a synthesis process at step 510. If the user enters F3 the system loads a process from a disk at step 512. If the user enters F4 the system saves an entered or edited process to disk at step 514. If the user selects F5 the current

process is displayed at step 516 while selection of F6 starts the main portion of the program, i.e., the actual synthesis according to the selected process. If the user selects F7 the system displays the location of the synthesized peptides, while pressing F10 returns the user to the disk operating system.

Please replace the paragraph beginning on page 20, line 21 with the following amended paragraph:

Fig. 5[b]B illustrates the synthesis step 518 in greater detail. The main loop of the program is started in which the system first moves the mask to a next position at step 526. During the main loop of the program, necessary chemicals flow through the reaction cell under the direction of the on-board computer in the peptide synthesizer. At step 528 the system then waits for an exposure command and, upon receipt of the exposure command exposes the substrate for a desired time at step 530. When an acknowledge of exposure complete is received at step 532 the system determines if the process is complete at step 534 and, if so, waits for additional keyboard input at step 536 and, thereafter, exits the perform synthesis process.

Please replace the paragraph beginning on page 27, line 1 with the following amended paragraph:

The recursive factoring of masks allows the products of a light-directed synthesis to be represented by a polynomial. (Some light activated syntheses can only be denoted by irreducible, i.e., prime polynomials.) For example, the polynomial corresponding to the top synthesis of Fig. 9[a]A (discussed below) is

$P = (A + B)(C + D)$

A reaction polynomial may be expanded as though it were an algebraic expression, provided that the order of joining of reactants X_1 and X_2 is preserved ($X_1X_2 \neq X_2X_1$), i.e., the products are not commutative. The product then is AC + AD + BC + BD. The polynomial explicitly specifies the reactants and implicitly specifies the mask for each step. Each pair of parentheses demarcates a round of synthesis. The chemical reactants of a round (e.g., A and B) react at nonoverlapping sites and hence cannot combine with one another [other]. The synthesis area is divided equally amongst the elements of a round (e.g., A is directed one-half

of the area and B to the other half). Hence, the masks for a round (e.g., the masks m_A and m_B) area orthogonal and form an orthonormal set. The polynomial notation also signifies that each element in a round is to be joined to each element of the next round (e.g., A with C, A with D, B with C, and B with D). This is accomplished by having m_C overlap m_A [an] and m_B equally, and likewise for m_D. Because C and D are elements of a round, m_C and m_D are orthogonal to each other and form an orthonormal set.

Please replace the paragraph beginning on page 31, line 6 with the following amended paragraph:

A four-step synthesis is shown in Fig. 9[a]A. The reactants are the ordered set {A, B, C, D}. In the first cycle, illumination through m_1 activates the upper half of the synthesis area. Building block A is then added to give the distribution 602. Illumination through mask m_2 (which activates the lower half), followed by addition of B yields the next intermediate distribution 604. C is added after illumination through m_3 (which activates the left half) giving the distribution 604, and D after illumination through m_4 (which activates the right half), to yield the final product pattern 608 {AC, AD, BC, BD}.

Please replace the paragraph beginning on page 31, line 19 with the following amended paragraph:

The above masking strategy for the synthesis may be extended for all 400 dipeptides form the 0 naturally occurring amino acids as shown in Fig. 9[b]B. The synthesis consists of two rounds, with 20 photolysis and chemical coupling [cycler] cycles per round. In the first cycle of round 1, mask 1 activates $1/20^{th}$ of the substrate for coupling with the first of 20 amino acids. Nineteen subsequent illumination/coupling cycles in round 1 yield a substrate consisting of 20 rectangular stripes each bearing a distinct member of the 20 amino acids. The masks of round 2 are perpendicular to round 1 masks and therefore a single illumination/coupling cycle in round 2 yields 20 dipeptides. The 20 illumination/coupling cycles of round 2 complete the synthesis of the 400 dipeptides.

Please replace the paragraph beginning on page 33, line 28 with the following amended paragraph:

The fifteen most highly labeled peptides in the array obtained with the synthesis of 1,024 peptides described above, were YGAFLS (SEQ ID NO:4), YGAFS (SEQ ID NO:5), YGAFL (SEQ ID NO: 6), YGGFLS (SEQ ID NO:7), YGAF (SEQ ID NO:8), YGALS (SEQ ID NO:9), YGGFS (SEQ ID NO:10), YGAL (SEQ ID NO:11), YGAFLF (SEQ ID NO:12), YGAF (SEQ ID NO:8), YGAFF (SEQ ID NO:13), YGGLS (SEQ ID NO:14), YGGFL (SEQ ID NO:15), YGAFSF (SEQ ID NO:16), YGAFLSF (SEQ ID NO:17). A striking feature is that all fifteen begin with YG, which agrees with previous work showing that an amino-terminal tyrosine is a key determinant of binding. Residue 3 of this set is either A or G, and residue 4 is either F or L. The exclusion of S and T from these positions is clear cut. The finding that the preferred sequence is YG (A/G) (F/L) fits nicely with the outcome of a study in which a very large library of peptides on phage generated by recombinant DNA methods was screened for binding to antibody 3E7 (see Cwirla et al., Proc. Natl. Acad. Sci. USA, (1990) 87:6378, incorporated herein by reference). Additional binary syntheses based on leads from peptides on phage experiments show that YGAFMQ (SEQ ID NO:18), YGAFM (SEQ ID NO:19), and YGAFQ (SEQ ID NO:20) give stronger fluorescence signals than does YGGFM (SEQ ID NO:21), the immunogen used to obtain antibody 3E7.